WHAT IS CLAIMED IS:

1. A transgenic nonhuman animal comprising at least one nonfunctional allele of a beta-secretase-1 (BACE-1) gene.

2. The transgenic nonhuman animal of claim 1 that is homozygous for the allele.

3. The transgenic nonhuman animal of claim 1 that is a rodent.

4. The transgenic nonhuman animal of claim 1 that is a mouse.

5. The transgenic animal of claim 1, wherein the animal or an ancestor thereof was produced by homologous recombination between an endogenous allele of the gene and a construct containing a positive selection marker flanked by segments showing sufficient sequence relatedness to the gene for the construct to recombine with the endogenous allele introducing the positive selection marker into the endogenous allele and rendering it nonfunctional.

6. The transgenic animal of claim 1, wherein the animal or an ancestor thereof was produced by homologous recombination between an endogenous allele of the gene and a construct containing a positive selection marker flanked by segments showing sufficient sequence relatedness to the gene to undergo homologous recombination with it, these segments being flanked by frt recombination sites, whereby the construct recombines with the endogenous gene introducing the positive selection marker and frt recombination sites into the endogenous allele, and the frt recombination sites undergo recombination with each other thereby excising DNA between the flp recombination sites resulting in a deleted nonfunctional form of the endogenous allele.

7. The transgenic nonhuman animal of claim 1, wherein the allele is rendered nonfunctional by deletion of at least a segment of an exon of the gene.

8. The transgenic nonhuman animal of claim 1, wherein the allele is rendered nonfunctional by deletion of at least a segment from exon 1 of the gene.

9. The transgenic nonhuman animal of claim 8, wherein the allele is rendered nonfunctional by homologous recombination with a targeting vector comprising a a lambda KOS genomic clone of BACE-1.

10. The transgenic nonhuman animal of claim 9, wherein the lambda KOS genomic clone comprises a BACE-1 nucleic acid from murine strain 129/SvEv covering 5.5 kb upstream and 2 kb downstream of exon 1.

11. The transgenic nonhuman animal of claim 2, wherein the allele is rendered nonfunctional by a 165 base pair deletion of exon 1 starting from 2 basepairs past the initiating methionine and extending through the end of exon 1 replaced with an expression casette in the targeting vector electroporated into 129 ES cells used to generate the transgenic nonhuman animal.

12. The transgenic nonhuman animal of claim 1, wherein the allele is rendered nonfunctional by deletion of exons 4-8.

13. The transgenic nonhuman animal of claim 1, further comprising a transgene comprising a mutation in the APP gene associated with familial Alzheimer's disease.

14. The transgenic nonhuman animal of claim 13, wherein the transgene comprises a mutation at codons 595 and 596 of human APP695, or an isoform or fragment thereof, wherein the amino acid residues at positions corresponding to positions 595 and 596 are asparagine and leucine, respectively.

15. The transgenic nonhuman animal of claim 13, wherein the transgene comprises a mutation at codon 717 of APP770 or an isoform or fragment of APP770 having a mutant amino acid residue at position 717.

16. The transgenic nonhuman animal of claim 13, wherein the mutant amino acid residue is isoleucine, phenylalanine or glycine.

17. The transgenic nonhuman animal of claims 13, wherein the animal is homozygous for the non-functional allele.

18. The transgenic nonhuman animal of claim 13, wherein the animal is heterozygous for the transgene.

19. A cortical cell culture derived from the transgenic animal of claim 1.

20. The cortical cell culture of claim 19, wherein the cell culture is a primary cell culture.

21. The cortical cell culture of claim 19, wherein the cell culture comprises a detectable amount of a peptide recognized by an antibody that recognizes residues 13-28 of Aβ.

22. A method for screening for an inhibitor of the production by a protease other than beta-secretase ("non-beta-secretase protease") of a peptide recognized by an antibody that recognizes residues 13-28 of Aβ, comprising

exposing the transgenic animal of claim 1 or a cortical cell culture derived therefrom to an agent, and

detecting the peptide produced in the transgenic animal or cell culture exposed to the agent,

wherein a reduced amount of peptide produced in the exposed transgenic animal or cell culture relative to a transgenic animal or cell culture which has not been exposed to the agent is indicative of inhibitory activity.

23. The method of claim 22, wherein a cortical cell culture is exposed to the agent.

24. The method of claim 22, wherein the cortical cell culture is a primary cell culture.

25. A method of analyzing potential side-effects for an inhibitor of beta-secretase, comprising

exposing a transgenic animal of claim 1 or a cortical cell culture derived therefrom to an inhibitor of beta secretase;
measuring whether there is a change in the level of at least one component of the transgenic animal or cortical cell responsive to the administration of the inhibitor; wherein a change in the level of at least one component indicates a potential side effect.

26. The method of claim 25, wherein the measuring step measures changes in the levels of a plurality of mRNA species.

27. An embryonic stell cell comprising at least one nonfunctional allele of a beta-secretase-1 (BACE-1) gene.

28. The embryonic stem cell of claim 27 that is homozygous for the allele

29. The embryonic stem cell of claim 27 that is a mouse embryonic stem cell.

30. The embryonic stem cell of claim 27 produced by homologous recombination with a targeting vector designed in a way that, upon homologous recombination, exons 4 to 8 of the BACE-1 gene are flanked with FLP recombinase target sites (frt sites).

31. The embryonic stem cell of claim 30, produced by homologous recombination with a targeting vector designed in a way that, with respect to the genomic locus, the 5' region of homology covered 4.5 kb and the 3' region 4.3 kb until the third frt site, and an additional 1.5 kb further 3'.

32. The embryonic stem cell of claim 27 that is homoygous for a nonfunctional allele lacking exons 4-8 of BACE-1.

33. The embryonic stem cell of claim 27, produced by homologous recombination with a first targeting vector that introduces a neomycin resistance gene in the BACE-1 gene and with a second targeting vector that replaces the neomycine resistance gene with a a hygromycin resistance gene cassette.

34. A blastocyst formed by differentiation of an embryonic stem cell as described in claim 27.